- Introduction
- Background
  - Pose estimation – what is it? Why is it important? Etc.
  - Data we will be using
  - Network structures (e.g., Why we choose RTMPose over HRNet?)
- What work was done?
  - Subset-based training
    - We decided to train on three different subsets (Bovidae, Bovidae+Cervidae, Entire AP10k) on the RTMPose model
    - The datasets were all reduced to match the size of the Bovidae set, to ensure the size of the dataset was not an active factor in our experiment
    - We excluded Antelopes from the training and validation sets due to a lack of images (200)
    - Testing is done on 100 set-aside antelope images that were consistent across all model testing
    - There are also 100 set-aside images of antelopes to finetune the models
    - We found that the addition of Cervidae images improved average precision, whereas the addition of all species in the AP10k dataset didn't improve performance by much. As such we see a correlation between adding similar-looking images to the training set to improve performance. This correlation can be further studied by continuing to vary the training set with similar images and adjusting the species distribution (ex: 30% argali sheep to 10%) within the dataset to explore the effects.
  - Keypoint definitions
    - Objective: Improve pose estimation model accuracy on more challenging data
    - AP10k dataset does not have a publicly available labeling scheme and many of their keypoints had high inconsistency
    - Decided to develop a custom labeling scheme, to ensure both consistency across our labelers and robustness for every keypoint
    - Ran into issues with ensuring consistency for the hip and neck keypoints
    - Decided to label two distinct points, and then interpolate the originally defined keypoint
      - Instead of labeling the neck keypoint in the middle of the neck, we labeled throat and wither keypoints, with the neck keypoint being calculated as the midpoint in preprocessing
      - Similiar process for the shoulder
      - Hip keypoint was interpolated from the root-of-tail keypoint and a keypoint marking the edge between the leg and the torso
    - Also had issues with the root-of-tail keypoint, so after multiple iterations, we decided on labeling the base of the tail, and added images in various angles to further clarify
    - Validated consistency of the keypoint definitions through trials with our labelers, and iteratively improved the definitions based on their feedback.

- - - Labeling effort
      - Used LabelMe software
    - Species similarity
    - Depth measure
    - etc.
    - (this is where you can document all the work/ideas you have)
- Potential future work

- (Appendix) - Each individual: a short paragraph about your work in the team
  - Medha - I began familiarizing myself with the project's scope, by first analyzing the AP10k, OpenPose, and AnimalPose research papers. Once I got a feel for the kind of work already done in the field, I started looking into the two main models in contention for our project (HRNet and RTMPose), by quantitatively comparing the model output on the Senegal Antelope dataset. As a group, once we decided to move forward with RTMPose, I began work on creating a keypoint definition proposal for labeling the Senegal Antelopes. I worked with Claire, to further refine these points, specifically working on the neck and root of tail keypoints. Through feedback from labeling using the definitions, we iteratively edited the definitions, till we had a finalized definition that was relatively consistent across labelers. We continued to label the images while doing other work. The next part of the project was training, so I worked on top of Josh's existing parsing script to extract training, validation, and testing annotated data, and then began training. I trained a bovidae+cervidae model, by using the existing parsing script to create a new dataset of training and validation, containing only animals of the bovidae and cervidae species. I created a new parsing script to extract the antelope images to create a constant testing and finetuning dataset, for all future models to be tested on. Afterward, I wrote a script to reduce the size of the bovidae+cervidae training and validation sets to match the size of the smaller bovidae-only data. I retrained the model and ran inferencing on sample images to have a visual comparison to other models. On the documentation side, I worked on the abstract and poster drafts and also kept a log of the commands used for training, testing, and inferencing on GitHub.

Resource:
- Weekly meetings
- Poster abstract and draft
- Talks in slack channel